IN THE UNITED STATES DISTRICT COURT
FOR THE MIDDLE DISTRICT OF GEORGIA
ATHENS DIVISION

UNITED STATES OF AMERICA,	:	
	:	
v.	:	**CRIMINAL NO. 3:21-CR-9 (CAR)**
	:	
CEDDRICK DEMON MERCERY,	:	
	:	
Defendant.	:	
	:	

United States' Response in Opposition to Defendant's Motion to Exclude DNA Evidence and Request for a *Daubert* Hearing

The United States of America ("the Government"), through undersigned counsel, hereby responds to "Defendant Ceddrick Mercery's Motion to Exclude or Limit Expert Testimony from Government DNA Expert Elizabeth Talley or in the alternative for a *Daubert* hearing." Defendant's motion is meritless and fails to address with requisite specificity the reliability, validity, and admissibility of the DNA analysis methodology used in this particular case. As a result, a hearing is neither required nor warranted, and Defendant's motion should be denied.

I. Introduction

a. Procedural and Factual History

On February 10, 2021, Defendant was indicted in the above-styled case for two counts of Possession of a Firearm by a Convicted Felon in violation of Title 18, United States Code, Sections 922(g)(1) and 924(a)(2). Doc. 1. On July 8, 2021, a superseding indictment was returned which added Count Three charging Possession of a Firearm by a Convicted Felon. Doc. 26. On February 9, 2022, a second superseding indictment was returned which added Count Four charging Possession of a Firearm by a Convicted Felon. Doc. 53.

In Count Two of the second superseding indictment, Defendant is charged with possessing a Glock, Model: 22, .40 caliber pistol that was located by law enforcement in an apartment in Athens on October 26, 2020. The seized Glock pistol was sent to the FBI laboratory in Quantico, VA, where it was tested for DNA. A swabbing of the textured area of the pistol's grip revealed the presence of male DNA, which "was interpreted as originating from three individuals." When the DNA from the pistol's grip was compared to Defendant's DNA, FBI DNA Forensic Examiner Elizabeth Talley ("FE Talley") concluded that the DNA located on the pistol's grip was "210 octillion times more likely if MERCERY and two unknown, unrelated people are contributors than if three unknown, unrelated people are contributors."

A state search warrant for Defendant's Instagram account was obtained by ACCPD Sgt. Dana Frost, which revealed photographs of Defendant brandishing the Glock pistol charged in Count Two. On September 3, 2021, Defendant filed a motion to suppress challenging the warrant for his Instagram account. Doc. 31. The Court granted Defendant's motion to suppress in a written order on February 25, 2022. Doc. 55. Defendant did not promptly move for a *Daubert* hearing or otherwise challenge the DNA evidence in his case when he filed his bevy of pretrial motions in 2021. Instead, Defendant waited until 45 days from the start of his trial to file the instant motion.

Because Defendant's motion is unsupported by anything impugning the methods used in this case, it should be summarily denied. In fact, Defendant's *barebones* motion does not even reference the probabilistic genotyping software that was used in his case, STRmix™. Defendant's motion merely cites a single New York state appellate opinion, *People v. Thompson*, 118 N.Y.S.3d 383 (N.Y. Sup. Ct. 2019), for the proposition that DNA identification can potentially be unreliable when multiple individuals are involved. As tacitly admitted in a footnote in Defendant's motion, the DNA genotyping technology addressed in *Thompson* was not STRmix. However, Defendant's

motion fails to reference New York opinions issued after *Thompson* which found STRmix to be highly reliable.[1]

As discussed below, courts have consistently upheld the reliability and admissibility of the STRmix software, which "is currently in use in over forty states and federal laboratories in the United States and in at least thirteen other countries." *United States v. Tucker*, 2020 WL 93951, at *4 (E.D.N.Y. Jan. 8, 2020). Expert testimony based on STRmix results is "overwhelmingly admitted" in American courts, *id.*, and "STRmix is the 'most tested and most…peer reviewed' probabilistic genotyping software available," *United States v. Gissantaner*, 990 F.3d 457, 465 (6th Cir. 2021) (citation omitted).

b. Explanation of Probabilistic Genotyping

Perhaps to create confusion and push the Court to hold an evidentiary hearing, Defendant does not explain what probabilistic genotyping and STRmix are. Even a rudimentary understanding, as set forth below, reveals that a hearing is unnecessary in this case.

i. DNA Basics – Loci and Alleles

A person's mother contributes half of one's DNA, and a person's father the other half. An individual's DNA is unique. No one else shares it, apart from an identical twin. Certain

[1] *See generally People v. Bullard-Daniel*, 163 N.Y.S.3d 726, 728-29 (N.Y. App. Div. 2022) (writing "Defendant further contends that the court erred in permitting the People to introduce the results of an analysis of the DNA material using the STRmix DNA analysis program (STRmix program) because such testing is not generally accepted by the relevant scientific community. We reject that contention…We conclude that the People established that the methods employed in the STRmix program were generally accepted as reliable within the relevant scientific community at the time the DNA evidence was analyzed (see generally *729 Wesley, 83 N.Y.2d at 422, 611 N.Y.S.2d 97, 633 N.E.2d 451; *People v. Wilson*, 192 A.D.3d 1379, 1380-1381, 143 N.Y.S.3d 466 [3d Dept. 2021]; *People v. Wakefield*, 175 A.D.3d 158, 162-163, 107 N.Y.S.3d 487 [3d Dept. 2019], lv granted 35 N.Y.3d 1097, 131 N.Y.S.3d 299, 155 N.E.3d 792 [2020]), and thus the court did not err in concluding that the results of the DNA analysis were admissible. We have considered defendant's remaining contention concerning the STRmix program, and we conclude that it lacks merit.")).

spots on the human genome, called "loci," contain segments of DNA code that vary widely from one person to another. Each variation is called an "allele," and a person generally has two alleles at each locus. A greater number of matching alleles at a greater number of loci increases the probability that a particular person of interest contributed the sample.

ii. Evolution of DNA Analysis Techniques

In the early years of working with DNA, forensic scientists used visual comparison to examine DNA samples. This presented a challenge to scientists examining DNA mixtures of several people because, at each locus, each person might have contributed zero, one, or two alleles. Additionally, the examiner might over-count or under-count the percentage of each individual's contribution to the mixture or mistake the number of people who contributed to it.

Starting in the late 1990s, i.e., more than 20 years ago, forensic scientists developed software products to improve analyses of multi-person DNA samples. This technology combines the tools of DNA science, statistics, and computer programming to mitigate the risks of subjective assessment. Using this approach, forensic scientists upload raw data representing the DNA sample into software that calculates the likelihood that a suspect's DNA profile is part of the sample, versus a random member of the population. If an analyst remains unsure whether a sample contains the DNA of three persons or four, she can use the software to crunch the numbers both ways.

iii. STRmix Generally

Today, forensic laboratories use a variety of sophisticated and tried-and-true probabilistic genotyping software programs. The product used in this case, STRmix, has undergone substantial testing by its developer (known as "developmental validation") to convince the scientific community the product works and may be reliably used. Developmental validation of probabilistic

genotyping software addresses, among other things, sensitivity, specificity, precision, and accuracy. STRmix's developmental validation study was published in a peer-reviewed journal six years ago.[2]

STRmix has also been "internally validated" by each of the dozens of laboratories that use it. Internal validation is the accumulation of test data within a laboratory to demonstrate that the established parameters, software settings, formulae, algorithms, and functions perform as expected. STRmix is currently used in 65 laboratories within the United States and more than 20 laboratories abroad. This means that 65 laboratories within the United States alone have separately tested STRmix and found it to reliably produce accurate results. FBI completed its original internal validation of STRmix in 2015 and published its validation in a peer-reviewed journal.[3]

The use of STRmix has been the subject of almost 90 peer-reviewed articles. The Government is unaware of any peer-reviewed article disproving the reliability of STRmix. As many courts have recognized, STRmix enjoys broad and general acceptance in the scientific community. *See, e.g.*, *United States v. Lewis*, 442 F. Supp. 3d 1122, 1155 (D. Minn. 2020) ("[T]here is no doubt that STRmix has gained general acceptance."); *United States v. Washington*, 2020 WL 3265142, at *2 (D. Neb. June 16, 2020) ("Authority and evidence demonstrate that STRmix is generally accepted by the relevant community."); *United States v. Christensen*, 2019 WL 651500, at *2 (C.D. Ill. Feb. 15, 2019) ("STRmix has been repeatedly tested and widely accepted by the scientific community."); *United States v. Pettway*, 2016 WL 6134493, at *1

[2] Jo-Anne Bright, et al., *Developmental Validation of STRmix, Expert Software for the Interpretation of Forensic DNA Profiles*, Forensic Science International: Genetics (2016), at 23:226-239.

[3] Tamyra R. Moretti, et al., *Internal Validation of STRmix for the Interpretation of Single Source and Mixed DNA Profiles* (2017), available at pubmed.ncbi.nlm.nih.gov/28504203.

(W.D.N.Y. Oct. 21, 2016) ("the scientific foundations of the STRmix process are based on principles widely accepted in the scientific and forensic science communities").

iv. The DNA at issue in this case

In this case, the FBI laboratory analyzed evidentiary swabs taken from the grip of the Glock pistol found in the Athens' apartment where Defendant was located on October 26, 2020, and a DNA sample (buccal swab) taken from Defendant. Each of the swabs then proceeded through the extraction, concentration, quantitation, amplification, and separation steps of DNA analysis. After the completion of these steps, an FBI forensic examiner imported the raw data produced during the separation process into STRmix and concluded that the swabs taken from the grip of the Glock pistol contained a mixture of male DNA suitable for comparison purposes.

FBI FE Talley then took the raw data representing the DNA present in the mixture and entered it into STRmix. With the goal of ascertaining the statistical probability that Defendant Mercery contributed DNA to the mixture, FE Talley used STRmix to compare Defendant's DNA profile to the raw data obtained from the Glock pistol.

FE Talley concluded the resulting DNA mixture originated from three individuals, one of whom was Defendant Mercery. The STRmix revealed that the DNA results from the Glock pistol were "210 octillion times more likely if Ceddrick Demon Mercery and two unknown, unrelated people were contributors than if three unknown, unrelated people were contributors." In other words, the DNA profile is 210 octillion times more likely if Defendant Mercery is a contributor, than if he is not. Not surprisingly based upon this finding, FE Talley documented in her report that there was "very strong support" that Defendant Mercery contributed to the DNA mixture found on the Glock pistol.

II. Legal Standard

An expert may testify about scientific knowledge if the expert's scientific, technical, or other specialized knowledge will help the trier of fact to understand the evidence or to determine a fact in issue; the testimony is based on sufficient facts or data; the testimony is the product of reliable principles and methods; and the expert has reliably applied the principles and methods to the facts of the case. Fed. R. Evid. 702. "Four inquiries guide the reliability analysis: Is the technique testable? Has it been subjected to peer review? What is the error rate and are there standards for lowering it? Is the technique generally accepted in the relevant scientific community?" *Gissantaner*, 990 F.3d at 463 (citing *Daubert v. Merrell Dow Pharms*., Inc., 509 U.S. 579, 593-94 (1993)).

Daubert hearings are not required before a judge may admit expert testimony. *United States v. Hansen*, 262 F.3d 1217 (11th Cir. 2001). *Daubert* hearings are not required but may be helpful in "complicated cases involving multiple expert witnesses." *City of Tuscaloosa*, 158 F.3d at 564–65 n. 21 (11th Cir. 1998). The trial court should conduct a *Daubert* inquiry when the opposing party's motion for a hearing is supported by "conflicting medical literature and expert testimony." *Tanner v. Westbrook*, 174 F.3d 542, 546 (5th Cir.1999). Consistent with *Daubert*, the evidence must be scientifically related to the disputed facts at issue in the case. *Allison v. McGhan Med. Corp*., 184 F.3d 1300, 1312 (11th Cir.1999). "[W]hen expert testimony is based upon such well-established principles, a defendant must do more than file a generic motion to merit an evidentiary hearing." *United States v. Campbell*, 2012 WL 2374528, at *6 (N.D. Ga. Apr. 19, 2012), report and recommendation adopted, 2012 WL 2373037 (N.D. Ga. June 22, 2012).

Here, Defendant Mercery's motion is generic and completely lacking in substance. It does not point to any significant adverse case law, literature, or expert testimony in support of its bold

assertion that the DNA evidence should be excluded or that in the alternative his case merits a *Daubert* hearing.

III. Argument

a. The DNA Evidence is Admissible

i. Testability

When an expert's methods and results are "discernible and rooted in real science—i.e., [are] 'intellectually rigorous'—they [are] empirically testable." *Quiet Tech. DC-8, Inc. v. Hurel-Dubois UK Ltd*., 326 F.3d 1333, 1346 (11th Cir. 2003) (quoting *Kumho Tire Co. v. Carmichael*, 526 U.S. 137, 152 (1999)). The question "is whether a method can be assessed for reliability, not whether it always gets it right." *Gissantaner*, 990 F.3d at 464 (internal quotation marks omitted).

With respect to DNA analysis methodologies, the Eleventh Circuit has noted that "[v]alidation studies go to the heart of reliability." *United States v. Barton*, 909 F.3d 1323, 1334 (11th Cir. 2018). STRmix can be, and has been, extensively tested through validation studies. Using lab-created DNA mixtures, in which the actual contributors of the DNA samples are known, scientists in over 65 American forensic laboratories, as well as the laboratories of 14 foreign countries, have separately tested STRmix. As the Sixth Circuit explained earlier this year:

> STRmix can be tested. Using "lab-created mixtures," in which the actual contributors of the DNA samples are known, scientists have tested STRmix to gauge the reliability of the technology. Suppose that one person, Aaron, contributed to a lab-created mixture, but another, Britney, did not. Forensic scientists can test STRmix to see whether it suggests that Aaron is a match for the mixture, but Britney is not. If STRmix suggests that Aaron is not a match for the mixture (by outputting a low likelihood ratio), that would be a false negative. If STRmix suggests that Britney is a match for the mixture (by outputting a high likelihood ratio), that would be a false positive. Each possibility shows that STRmix is testable, that lab-created mixtures offer a way to "assess[ ] [the] reliability" of STRmix.

Gissantaner, 990 F.3d at 464 (internal citation omitted).

Moreover, as set forth below, STRmix is not merely testable but it has been tested – repeatedly – and found to be reliable – repeatedly – for use in forensic casework.

ii. Peer Review

When scientific research is accepted for publication by a reputable journal following the "usual rigors of peer review," that represents "a significant indication that it is taken seriously by other scientists, i.e., that it meets at least the minimal criteria of good science." *Daubert v. Merrell Dow Pharms., Inc.*, 43 F.3d 1311, 1318 (9th Cir. 1995).[4] "STRmix is the 'most tested and most…peer reviewed' probabilistic genotyping software available." *Gissantaner*, 990 F.3d at 465. *See also United States v. Washington*, 2020 WL 3265142, at *2 (D. Neb. June 16, 2020) ("[C]ourts have recognized that STRmix software has been thoroughly tested and reviewed."); *Pettway*, 2016 WL 6134493, at *2 ("The software and its underlying principles have been peer-reviewed in more than 90 articles.").

iii. Error Rate and Standards to Lower it

Daubert's third factor looks to whether the scientific community has established standards that forensic scientists can use to mitigate the risk of error. Other courts have documented that STRmix's error rate is exceedingly low. For example, when examining "false inclusions," a recent peer-reviewed study concluded, based on an analysis of the DNA of 300,000 profiles that were known not to be in a mixture, that STRmix accurately excluded the noncontributors 99.1% of the time.[5] In other words, in less than 1% of the time did STRmix produce a likelihood ratio suggesting

[4] "The scientific community uses different conventions for publication from most journals published in the legal community. . . . [I]t is one thing to convince lawyers in training to publish a piece; it is quite another to convince peers in a professional community to publish a piece." *Gissantaner*, 990 F.3d at 464.

[5] Sarah Noël, et al., *STRmix*™ Put to the Test: 300,000 Non-Contributor Profiles Compared to Four-Contributor DNA Mixtures and the Impact of Replicates, Forensic Science Int'l: Genetics 41 (2019), at 24-31.

that someone was included in the mixture who was not actually included in it. *Id.* Most of these false inclusions, moreover, were associated with low likelihood ratios—meaning that, under STRmix's own estimates, the confidence that the person was included was low. As the Sixth Circuit explained: "A likelihood ratio of 100 to 1 is more likely to produce a false inclusion than a likelihood ratio of 1 million to 1." *Gissantaner*, 990 F.3d at 465.[6]

The Sixth Circuit hypothesized that "[o]ne explanation for the low error rate is the existence of standards to guide the use of STRmix and other probabilistic genotyping software." *Id.* at 466. Indeed, respected scientific organizations such as the Scientific Working Group on DNA Analysis Methods ("SWGDAM") have established standards and guidelines for the validation and use of STRmix. And, the FBI has developed and follows additional quality assurance standards that require both a technical and administrative review of a DNA examiner's work before a report is issued.

iv. General Acceptance in the Scientific Community

Unquestionably, probabilistic genotyping software generally and STRmix specifically enjoy general acceptance in the scientific community. Indeed, "[g]eneral acceptance of probabilistic genotyping software…has led to its use in inculpatory and exculpatory settings alike." *Gissantaner*, 990 F.3d at 467. Examples abound, including in Georgia. For instance, probabilistic genotyping exonerated Kerry Robinson of a crime for which he served nearly two decades in prison. Joshua Sharpe, *DNA Analysis Frees Ga. Man Wrongfully Convicted of Rape After 18 Years*, Atl. J. Const. (Jan. 8, 2020). Months later, the Georgia Supreme Court affirmed that Johnny

[6] In this case, the likelihood ratios exceed the Sixth Circuit's "1 million to 1" example by a lot (and that is a gross understatement). Where one million has six (6) zeros, one octillion is followed by twenty-seven (27) zeros. With respect to the sample taken from the grip of the Glock, it is 210,000,000,000,000,000,000,000,000,000 times more likely that Defendant contributed to the mixture than two unknown, unrelated people.

Lee Gates was entitled to a new trial after serving 43 years of a life sentence, based on the results of probabilistic genotyping software that excluded Gates as a contributor to certain DNA mixtures. *See State v. Gates*, 840 S.E.2d 437 (Ga. 2020).

In his motion, Defendant Mercery cites no example of a court excluding STRmix results. The undersigned prosecutor is aware of only one such instance, but that resulted in a scathing reversal. *See United States v. Gissantaner*, 417 F. Supp. 3d 857 (W.D. Mich. 2019), rev'd, 990 F.3d 457 (6th Cir. 2021). As noted above, countless other courts have admitted STRmix over challenges to its general acceptance.

CONCLUSION

As the Sixth Circuit concluded last year, "[a]ll in all, STRmix satisfies Rule 702 and the case law construing it. In the words of Rule 702, it is the 'product of reliable principles and methods.'" *Gissantaner*, 990 F.3d at 467. For all of the reasons set forth above, the Court should reject Defendant's meritless motion and deny without a hearing Defendant's motion to preclude DNA evidence.

Respectfully submitted, this 27th day of July, 2022.

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CERTIFICATE OF SERVICE

I certify that I have this day filed the foregoing *United States' Response in Opposition to Defendant's Motion to Exclude DNA Evidence and Request for Daubert Hearing* utilizing the Court's CM/ECF program, which will cause electronic notice to be provided to:

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Respectfully submitted, this 27th day of July, 2022.

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